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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 17:57:20 EDT 2007

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Application No: 10728979 Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-07 09:28:31.766
Finished: 2007-06-07 09:28:33.424
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 658 ms
Total Warnings: 38
Total Errors: 0
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

Input Set:

Output Set:

Started: 2007-06-07 09:28:31.766
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Error code	Error Description
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SEQUENCE LISTING

<110> NEC CORPORATION
MIYAKAWA, Tomoya
NAKAZATO, Takeru
ASOGAWA, Minoru

<120> Sequence Display Method and Homogeneity Search Method

<130> Q78853

<140> 10728979
<141> 2007-06-07

<150> JP 2002-358407
<151> 2002-12-10

<150> US 10/728,979
<151> 2003-12-08

<160> 93

<170> PatentIn version 3.1

<210> 1
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<212> DNA
<213> Artificial Sequence

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1 5 10 15

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
20 25 30

gca ggt ccg ttc ccg ggg agc cag acc tcg gac acc ttg cct gaa gtt 144
Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

tcg gcc ata cct atc tcc ctg gac ggg cta ctc ttc cct cgg ccc tgc 192
Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

cag gga cag gac ccc tcc gac gaa aag acg cag gac cag cag tcg ctg 240
Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

tcg gac gtg gag ggc gca tat tcc aga gct gaa gct aca agg ggt gct		288	
Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala			
85	90	95	
gga ggc agc agt tct agt ccc cca gaa aag gac agc gga ctg ctg gac		336	
Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp			
100	105	110	
agt gtc ttg gac act ctg ttg gcg ccc tca ggt ccc ggg cag agc caa		384	
Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln			
115	120	125	
ccc agc cct ccc gcc tgc gag gtc acc agc tct tgg tgc ctg ttt ggc		432	
Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly			
130	135	140	
ccc gaa ctt ccc gaa gat cca ccg gct gcc ccc gcc acc cag cgg gtg		480	
Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val			
145	150	155	160
ttg tcc ccg ctc atg agc ccg tcc ggg tgc aag gtt gga gac agc tcc		528	
Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser			
165	170	175	
ggg acg gca gct gcc cat aaa gtg ctg ccc ccg ggc ctg tca cca gcc		576	
Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala			
180	185	190	
cgg cag ctg ctg ctc ccg gcc tct gag agc cct cac tgg tcc ggg gcc		624	
Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala			
195	200	205	
cca gtg aag ccg tct ccg cag gcc gct gcg gtg gag gtt gag gag gag		672	
Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu			
210	215	220	
gat agc tct gag tcc gag gag tct gcg ggt ccg ctt ctg aag ggc aaa		720	
Asp Ser Ser Glu Ser Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys			
225	230	235	240
cct ccg gct ctg ggt ggc gcg gct gga gga gca gcc gct tgt		768	
Pro Arg Ala Leu Gly Gly Ala Ala Gly Gly Gly Ala Ala Ala Cys			
245	250	255	
ccg ccg ggg gcg gca gca gga ggc gtc gcc ctg gtc ccc aag gaa gat		816	
Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp			
260	265	270	
tcc cgc ttc tca gcg ccc agg gtc gcc ctg gtg gag cag gac gcg ccg		864	
Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro			
275	280	285	
atg gcg ccc ggg cgc tcc ccg ctg gcc acc acg gtg atg gat ttc atc		912	
Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile			
290	295	300	
cac gtg cct atc ctg cct ctc aat cac gcc tta ttg gca gcc cgc act		960	

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr			
305	310	315	320
cgg cag ctg ctg gaa gac gaa agt tac gac ggc ggg gcc ggg gct gcc			1008
Arg Gln Leu Leu Glu Asp Ser Tyr Asp Gly Gly Ala Gly Ala Ala			
325	330	335	
agc gcc ttt gcc ccg ccg cg act tca ccc tgt gcc tcg tcc acc ccg			1056
Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro			
340	345	350	
gtc gct gta ggc gac ttc ccc gac tgc gcg tac ccg ccc gac gcc gag			1104
Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu			
355	360	365	
ccc aag gac gac gcg tac cct ctc tat agc gac ttc cag ccg ccc gct			1152
Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala			
370	375	380	
cta aag ata aag gag gag gaa ggc gcg gag gcc tcc gcg cgc tcc			1200
Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser			
385	390	395	400
ccg cgt tcc tac ctt gtg gcc ggt gcc aac ccc gca gcc ttc ccg gat			1248
Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp			
405	410	415	
ttc ccg ttg ggg cca ccg ccc ccg ctg ccg ccg cga gcg acc cca tcc			1296
Phe Pro Leu Gly Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser			
420	425	430	
aga ccc ggg gaa gcg gcg gtg acg gcc gca ccc gcc agt gcc tca gtc			1344
Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val			
435	440	445	
tcg tct gcc tcc tcg ggg tcg acc ctg gag tgc atc ctg tac aaa			1392
Ser Ser Ala Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys			
450	455	460	
gcg gag ggc gcg ccg ccc cag cag ggc ccg ttc gcg ccg ccg ccc tgc			1440
Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys			
465	470	475	480
aag gcg ccg ggc gcg agc ggc tgc ctg ctc ccg cgg gac ggc ctg ccc			1488
Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro			
485	490	495	
tcc acc tcc gcc tct gcc gcc gcc ggg ggc gcg gcc ccc gcg ctc tac			1536
Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr			
500	505	510	
cct gca ctc ggc ctc aac ggg ctc			1560
Pro Ala Leu Gly Leu Asn Gly Leu			
515	520		

<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> QUERY Polypeptide

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20 25 30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Cys
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser

420

425

430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
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500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu
515 520

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<211> 60
<212> DNA
<213> Artificial Sequence

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<210> 4
<211> 57
<212> DNA
<213> Unknown Sequence

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<210> 5
<211> 60
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<213> artificial

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<223> gi|35651|emb|X51730.1|HSPREC

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<210> 6
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<400> 6
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<210> 7
<211> 60
<212> DNA
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<223> gi|4505766|ref|NM Polynucleotide

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<223> gi|189934|gb|M15716.1|HUMPGRR Polynucleotide

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<212> DNA
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<223> gi|22759951|dbj|AB085845.1| Polynucleotide

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<210> 10
<211> 60
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<400> 10
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<210> 11
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<211> 60
<212> DNA
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<400> 12
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<210> 13
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<211> 60
<212> DNA
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